

IINA_SEQUENCE 1.0
 LOCUS AA639414 412 bp mRNA linear EST 23-OCT-1997
 DEFINITION ng89a12.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1159486 3',
 mRNA sequence.
 ACCESSION ~~AA639414.1~~
 VERSION AA639414.1 GI:2563193
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 412)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html
 Seq primer: -40m13 fwd. ET from Amersham.
 Location/Qualifiers
 1..412
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="1159486"
 /clone_id="NCI_CGAP_C09"
 /tissue_type="colon tumor RER+"
 /lab_host="DH10B"
 /note="Organ: colon; Vector: pT7AD-Pac (Pharmacia) with a
 modified polylinker; 1st strand cDNA was prepared from
 RER+ colon tumor, and was then primed with a Not I -
 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is not normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo (Soares4
)".
 BASE COUNT 84 a 129 c 117 g 82 t
 ORIGIN
 AA639414 Length: 412 May 23, 2003 18:23 Type: N Check: 7057 ..
 1 GGGAAATGCA CTTTATTGG ATTGGTTGG TGGGTTGGG GTCTCAGAC
 51 AAACTAGAAG GCCTTACATA GGCAGCTGGG CCCACAGACT GGGTTCCCTG
 101 ACCCAGGACT TCATTCTGGC CTGTCCCCC AAAGCATAGC CTCACCTTC
 151 TCACCTTCT CCAGAGGAGT CTCCTCCACC CCCACAGAGG CTGTGACAG
 201 GCCCTGCAGC CTTAGGGAAG GAGGAAGGCT CTTGCAAGTA GACACTAAGG
 251 CACAGCGGGG CCCAGGGGTC ATAAAGGCTC TTCTGGCGGT GGCATCTGCT
 301 GGGGCTTCCA GCTGGGCGAG GGCTCCAGCG AACCGCTGAC CATCCAGAG
 351 TAGTTTGGGT GCACCTGGCC CTGCACGGCC TCGCTAACCA TCAATTCCCC
 401 ATCCACTGCA AA

*Reverse
complement*

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TOIG of Reverse of aa639414 check: 7057 from: 1 to: 412
LOCUS      AA639414                412 bp    mRNA    linear    EST 23-OCT-1997
DEFINITION      ng89412.s1 NCI_CGAP_C09 Homo sapiens cDNA clone IMAGE:1159486 3',
                mRNA sequence.
ACCESSION      AA639414
VERSION        AA639414.1 GI:2563193
KEYWORDS
SOURCE        human.
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 412)
AUTHORS       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE         National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                Tumor Gene Index
JOURNAL       Unpublished (1997)
COMMENT       Contact: Robert Strausberg, Ph.D.
                Email: cgapbs-remail.nih.gov
                Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
                , Ph.D.
                cDNA Library Preparation: M. Bento Soares, Ph.D.
                cDNA Library Arrayed by: Greg Lennon, Ph.D.
                DNA Sequencing by: Washington University Genome Sequencing Center
                Clone distribution: NCI-CGAP clone distribution information can be
                found through the I.M.A.G.E. Consortium/BLNI at:
                www-bio.11nl.gov/dbfp/image/image.html
                Seq primer: -40m13 fwd. ET from Amersham.

FEATURES
Source
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        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_image="1159486"
        /clone_lib="NCI_CGAP_C09"
        /tissue_type="Colon tumor RER+"
        /lab_host="DH10B"
        /note="Organ: colon; Vector: pTZ19-Pac (Pharmacia) with a
        modified polylinker; 1st strand cDNA was prepared from
        RER+ colon tumor, and was then primed with a Not I -
        o1igo(dT) primer. Double-stranded cDNA was ligated to Eco
        RI adaptors (Pharmacia), digested with Not I and cloned
        into the Not I and Eco RI sites of the modified pTZ19
        vector. Library is not normalized. Library was
        constructed by Bento Soares and M. Fatima Bonaldo (Soares4
        )"
BASE COUNT      84 a      129 c      117 g      82 t
ORIGIN
AA639414 Length: 412 May 23, 2003 18:23 Type: N Check: 7057
TTTCAGATGATGGGGAATTGATGATTAGCGAGCCGTCAGAGGCCAGGTCACCCAACTACTTGTGA
TGTTCAGAGGTTGGGCGCTGCGACCTGAGAGCCCGACGATGCCACGCCAGAGAGCCCTT
ATGACCCCGTGGCGCGCTGCGCTAGTGTCTACTTCTGACGACCTCTCTCTCTCTAGGGCTGAGG
GCCGTCCACAGCTCTCTGTGGGGGAGACTCTCTGTGAGAGGGTGAGAGAGGTCGATGCT
TTGGGGGACAGGCGCAATTAATCTCTGGSTCAAGGAAACCCAGTCTGCTGGCCCGCATGTATGAG
GCCTTCTAGTTTGTGAGACCCACCCACGACCAATTCAAATTAAGTACATTCCTC
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[illegible]

File of reverse of: a1042283, check: 5240 from: 1 to: 447

LOCUS a1042283 447 bp mRNA linear EST 24-SEP-1998
DEFINITION oyl3e09.x1 Soares_senescent_fibroblasts_NBHSF Homo sapiens cDNA
clone IMAGE:1665736 3', mRNA sequence.
ACCESSION a1042283
VERSION a1042283.1 GI:3281477
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgap@r-email.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (infoimage.lnl.gov) for further information.
Insert Length: 693 Std Error: 0.00
Seq primer: -40m13 fwd. RT from Amersham
High quality sequence stop: 376.
Location/Qualifiers
1. 447
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1665736"
/clone_lib="Soares_senescent_fibroblasts_NBHSF"
/tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
TGTTACCAATCGAAGTGGAGCGCGCATTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 87 a 142 c 121 g 97 t
ORIGIN
a1042283 Length: 447 May 23, 2003 18:21 Type: N Check: 5240
a1042283
TGAGGCCAGAGATGGGAAGGTGTGTTCAGATGGATGGGAATGATGTTAGCGAGGCCGTGCAGGG
CCAGGTGCACCAACTTCTGTGATGTGATGTCAGCGGTGCGTGAGCCCGCCAGCTGGAAGCCCGAG
CAGATGCCACCCGACGAGAGAGCCCTTATGACCGCGCGCTGTGCTTGTACTGACGAGAC
CCTTCTCTCTCCCTAGAGGCGCTGACGAGCGCTGACACAGCTCCGTGAGGAGGAGAGACTCCTGAG
AAGGCTGAGAGAGAGGAGCTATGCTTGGGGGAGACAGGCGCAAGATGAGTCTCTGGGTCAGAGCCCGAC
TGCGCTGGGCGCCAGCTGCTATGAGGCTTCTAGTTTCTTCTGAGACCCCGACCCACGACCAATATCC
AATTAAGTGCATTCCCAAAAAAAAI

Sequence Name	Description	Length	Init. Opt. score	Sig. Frame
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[illegible]

a1042283 TOIG of reverse of: a1042283 check: 5240 from: 1

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Residue Identity = 98%
Matches          = 442
Gaps             = 0
Conservative Substitutions = 5
Mismatched       = 0

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GCCCGTGGTGCCCTTCGCGTTGGAGCCCCAAGATGGGAAGGTGTGTTGCACGTGGATGGGGAAATTGATGGT
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x	10	20	30	40	50
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1170 1180 1190 1200 1210 1220 1230

TAAGCAGGCGCTGCAGGCGCAGGTCGACCCAACTACTTCCTGGATGGTCAGCGCTCGTGGAGCCCCCGC

TAGCGAGGCCGTGCAGGGCCAGGTGCACCAACTACTTCTGGATGGTCAGCGTTGCCGTGGAGCCCCGCC

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130 140 150 160 170 180 190

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TCCTACTTGCAGGACCCCTCCTCCTTCCCTAGGGCTGCAGGGCCCTGTCCACAGCTCCTGTGGGGTGAGGAG

TTCTTACAGACCTCTTACGGCTGTCCACAGCTCCTGTGGGGGTGAGGAG

200 210 220 230 240 250 260

1390 1400 1410 1420 1430 1440 1450 .

[illegible]

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	1400	1470	1480	1500	1510	1520
CGAGGACATGGCCTCCATCATTCAGGCCTTCAAGACCTCCACCGAA						

350 360 370 380 390 400 410

1530 1540 1550 1560 1570

CCAAATCCAATAAGTGACATTCCCGCCTGAAAAAAAAAAAA

CCAATCCAATAAGTGACATTCGCCAAAAAAA

420	430	440	A
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	[FOLG Of:	a1042283	check:	5240	from:	1	to:	447	
LOCUS	A1042283-	447 bp	mRNA		linear			EST 24-SEP-1998	
DEFINITION	oyl13e09.x1 Soares_senescent_fibroblasts_NBHSF Homo sapiens CDNA clone IMAGE:1665736 3'		mRNA sequence.						
ACCESSION	A1042283								
VERSION	A1042283.1								
KEYWORDS	GI:3281477								
SOURCE	EST.								
ORGANISM	human.								
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 447) NCI-CGAP http://www.ncbi.nlm.nih.gov/cgi/gap.								
AUTHORS	National Cancer Institute, Cancer genome Anatomy Project (CGAP), Tumor Gene Index								
TITLE	Unpublished (1997)								
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapsr@email.nih.gov								
COMMENT	This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 693 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 376. Location/Qualifiers 1..447 /organism="Homo sapiens" /db_xref="taxon:9606" /cclone_lib="Soares_senescent_fibroblasts_NBHSF" /tissue_type="senescent fibroblast" /lab_host="DH10B (ampicillin resistant)" /note="Vector: pTZ19 (Pharmacia) with a modified polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco RI primer 15' TCCTACCAGATCGAAGTGGAAGCCGCCGCACAATTTTTTTTTTTTTT TTTT TT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."								
BASE COUNT	87 a 142 c 121 g 97 t								
ORIGIN									
	A1042283	Length: 447	May 23,	2003 16:21	Type: N	Check: 5240 ..			
	a1042283								
	TTTTTTTTGGGAATGTCACTTTATTATGGTAGTTGGTCTGGGGGTGGGGGTCTCAGAACAATACTAAAGG CATTACTAAGGAGCATGGGCCCCAGGCTGGGCTCTCACACAGACGATTAATCTGGCTGTCCCACCA AAGCTATACCTCTACCTCTCCCTCTCCAGAGAGAGTCTCTCACCCACCCACAGAGAGGTGGMGAGG CCTCTACAGCCCTTAGGAGGAGAGAGGAGGTCTGCGAACATGACATTAAGGACAGCGGCGCCAGGGCTCA TAAGGCTCTTTTGGCGGTGGCATCTGCTGGGGCTTCCAGCTGGGGGGGGCTCCACGCAACCTGTAC ACACGAAAGTACTTTGGGTGGAGCGCTCTCAGCGGCTCGCTAACATCAATCCCATCCATCCATGCA CAACACTTTTCCACTTGGGGCTCCA								

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-937-060a-19.res made by shanley on Wed 28 May 103 15:04:06-PDT.

Query sequence being compared: US-09-937-060a-19 (1-1573)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-937-060a-19 (1-1573) with:
File: 42283.rev.seq

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O -
F 10-
S -
E 5-
U -
N -
C -
S 0-
SCORE 0 49 98 146 195 244 293 341 390 439
STDEV

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PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 4
Gap penalty 5.00 Window size 30
Gap size penalty 0.33 500
Cutoff score 10
Randomization group 0

SEARCH STATISTICS

Scores: Mean 439 Median 0 Standard Deviation 0.00

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 447
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame
1. a1042283	TOIG of reverse of: a1042283	447	439	442 0.00 0
1. US-09-937-060a-19 (1-1573)				
a1042283	TOIG of reverse of: a1042283	check: 5240	from: 1	
Initial Score	= 439	Optimized Score	= 442	Significance = 0.00
Residue Identity	= 98%	Matches	= 442	Mismatches = 5
Gaps	= 0	Conservative Substitutions	= 0	
1100 1110 1120 1130 1140 1150 1160				
GCCCCGTGCGCTTCCGCTTGGAGCCCAAGATGGAGAAAGCTGTGTCAGTGTGAGGAAATGATGT				
TGGAGCCCAAGAGATGGAGAAAGCTGTGTCAGTGTGAGGAAATGATGT				
X 10 20 30 40 50				
1170 1180 1190 1200 1210 1220 1230				
TAGGAGAGCCGCTGAGAGGCCAGAGTGCACCAACTACTTCTGATGTGTCAGGCTTGGAGACCCCGCC				
TAGGAGAGCCGCTGAGAGGCCAGAGTGCACCAACTACTTCTGATGTGTCAGGCTTGGAGACCCCGCC				
60 70 80 90 100 110 120				
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CAGCTGGAGAGCCCGCAGAGATGCCACCGCCAGAGAGAGCCCTTATGACCCCTGAGCCCGCTGCTTATG				
CAGCTGGAGAGCCCGCAGAGATGCCACCGCCAGAGAGAGCCCTTATGACCCCTGAGCCCGCTGCTTATG				
130 140 150 160 170 180 190				
1320 1330 1340 1350 1360 1370 1380				
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TCTACTTGCAGAGACCCCTCCCTCCCTTCCCTAGAGGCTGAGAGGCTGTCACAGCTCTGTGGGGTGGAGAG				
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1390 1400 1410 1420 1430 1440 1450				
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ACTCTCTTGGAGAGGCTGAGAGAGTGTGAGAGGCTTGTGTTGGGGGACAGGCCCAAGATGAATGCTGGCTA				
270 280 290 300 310 320 330 340				
1460 1470 1480 1490 1500 1510 1520				
GGAGCCAGCTGGCTGGGCCAGCTGCTATGTAAGGCTTCTAGTGTGTCAGACCCCAACCCAGCA				
GGAGCCAGCTGGCTGGGCCAGCTGCTATGTAAGGCTTCTAGTGTGTCAGACCCCAACCCAGCA				
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1530 1540 1550 1560 1570				
CCAAATCCAAATTAAGTACATTCCTCCAGCCCTGAGAAAAA				
CCAAATCCAAATTAAGTACATTCCTCCAGCCCTGAGAAAAA				
420 430 440 X				

l!NA_SEQUENCE 1.0
 LOCUS AA639414 412 bp mRNA linear EST 23-OCT-1997
 DEFINITION ng89a12.s1 NCI-CGAP_C09 Homo sapiens cDNA clone IMAGE:1159486 3',
 mRNA sequence.
 ACCESSION @AA639414.1
 VERSION AA639414.1 GI:2563193
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 412)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
 Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
www.bio.lnl.gov/db/rdp/image/image.html
 Seq primer: -40m13 fwd. RT from Amersham.
 Location/Qualifiers
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 /note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
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 oligo(dT) primer. Double-stranded cDNA was ligated to Eco
 RI adaptors (Pharmacia), digested with Not I and cloned
 into the Not I and Eco RI sites of the modified pT73
 vector. Library is not normalized. Library was
 constructed by Bento Soares and M. Fatima Bonaldo (Soares4
)."
 BASE COUNT 84 a . 129 c 117 g 82 t
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 51 AACTATAGAG GCCTTACATA GGCAGCTGG CCCAGCAGCT GGGTTCCTG
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 151 TCACCTTCT CCAGAGAGT CTCTCCACC CCCACAGGAG CTGTGACAG
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 401 ATCCACTGCA AA

*Reverse
complement*

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DEFINITION ng89a12.s1 NCI-CGAP Co9 Homo sapiens cDNA clone IMAGE:1159486 3',
            mRNA sequence.
ACCESSION  AA639414
VERSION    AA639414.1 GI:2563193
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE  1 (bases 1 to 412)
            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
            Unpublished (1997)
JOURNAL    Contact: Robert Strausberg, Ph.D.
COMMENT    Email: cgapbs-remail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
            Ph.D.
            cDNA library Preparation: M. Bento Soares, Ph.D.
            cDNA library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: -40m13 fwd. ET from Amersham.
FEATURES   Location/Qualifiers
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                        vector. Library is not normalized. Library was
                        constructed by Bento Soares and M. Fatima Bonaldo (Soares4
                        )".
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